SUPPLEMENTAL FIGURE LEGENDS:

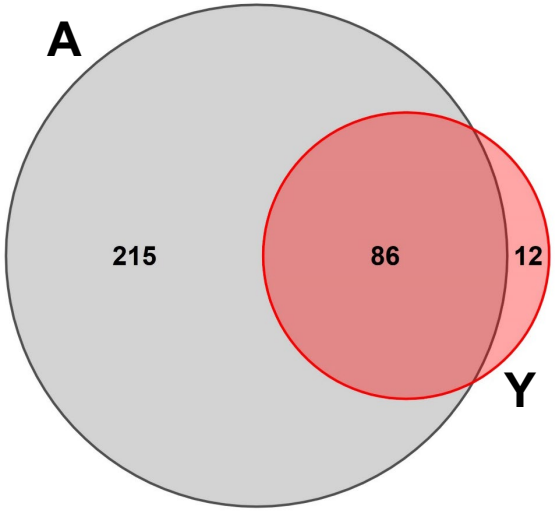
Suppl. Fig. 1 Distribution of gene ontology annotations for molecular functions of the identified proteins obtained from sEVs isolated from young vs aged peritoneal lavage.

Venn diagrams show the number of genes identified in aged (A) and young (Y) samples, categorized by gene ontology molecular function. Gray represents A samples, red represents Y samples

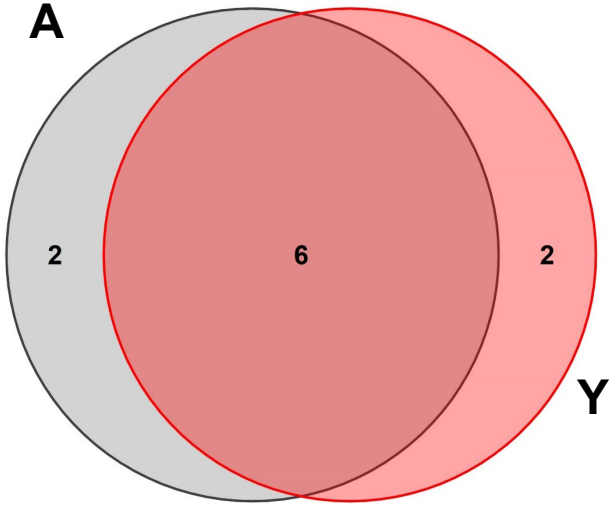
Suppl. Fig.2. Validation of sEV proteomic data using western blot analysis.

(A) Validation of proteins found only in the aged (A) EV proteomic data **(B)** Validation of **p**roteins found to be more highly expressed in the A proteomic dataset relative to the young (Y). Samples were electrophoresed on 9% SDS-polyacrylamide gels and electroblotted to immobilon membranes. After blocking with 5% milk, blots were incubated with primary antibody (1:100 dilution) followed by secondary antibody (1:4000) and developed using SuperSIgnal West Dura. Blots were visualized on a Bio-Rad ChemiDoc MP Imaging system.

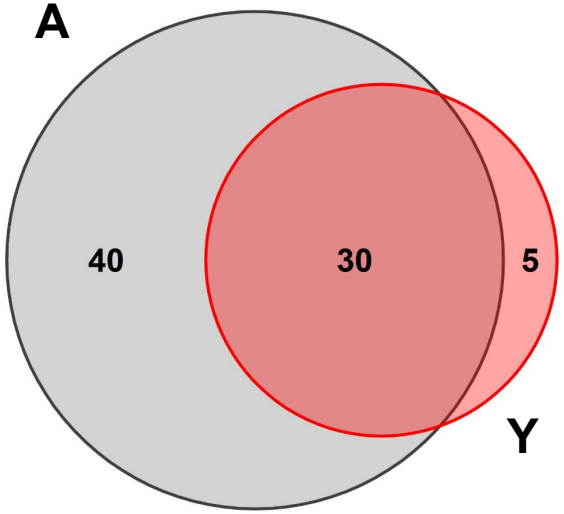
Total Binding Proteins A *vs.* Y



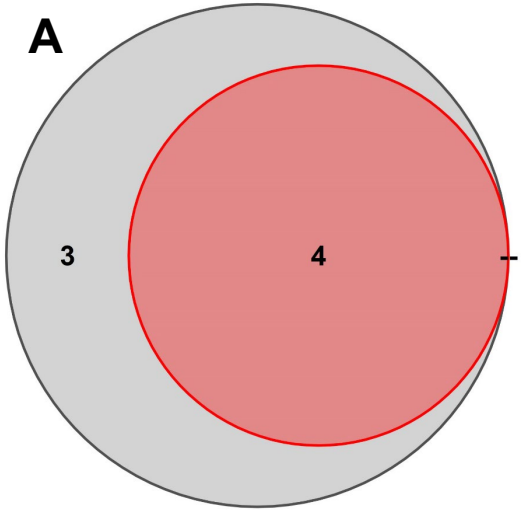
Cell Adhesion Proteins



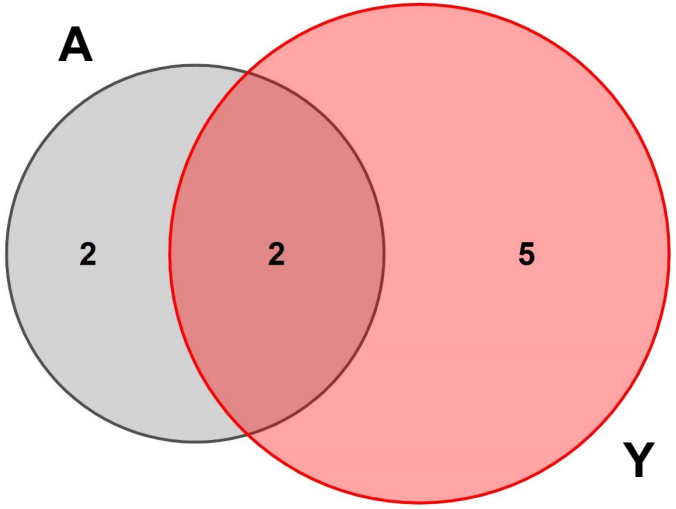
Protein Binding Activity Modulator



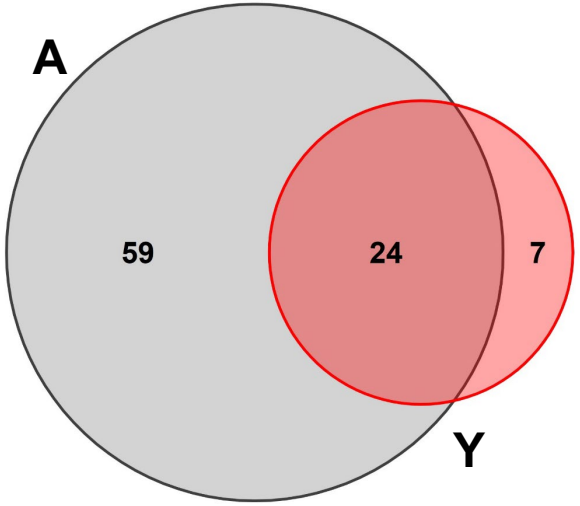
Intracellular Signal Protein



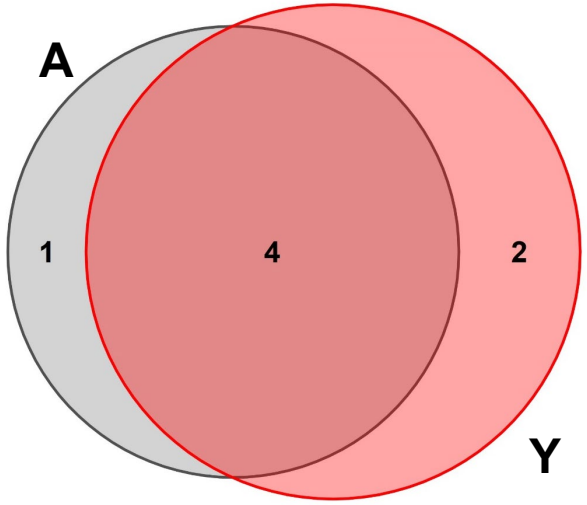
Extracellular Matrix Proteins



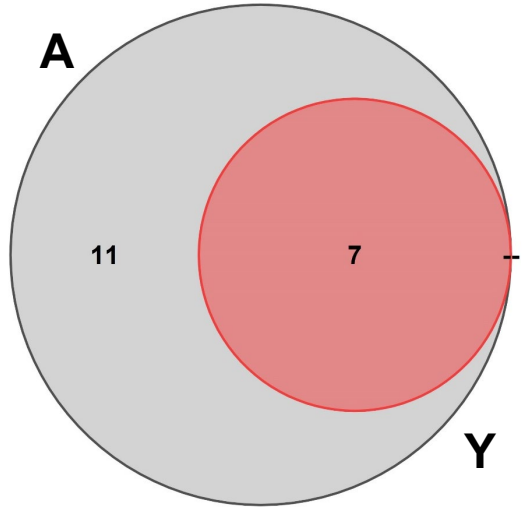
Defense Immune Proteins



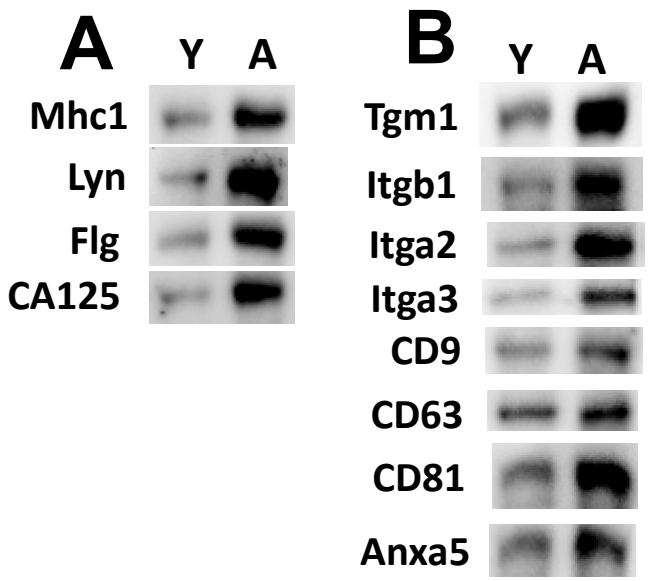
Transmembrane Signal Receptor



Chaperone



Suppl. Fig. 2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Y
A
Mhc1
Lyn
Flg
CA125
B
Y
A
Tgm1
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Anxa5